AMENDMENTS TO THE SPECIFICATION

At page 5 in the specification, please replace the paragraph spanning lines 7-17 with the following replacement paragraph:

Figure 2. Amino acid sequence alignment of members of SCP-2 gene family with AeSCP-2 (BQ785056; herein, SEQ ID NO:3). Human SCP-2 (NM_002979) (SEQ ID NO:6). Rat SCP-2 (M57454) (SEQ ID NO:5). Anopheles gambiae SCP-2 (EAA08376) (SEQ ID NO:4). Fruit fly C-terminal portion of SCP-X (X97685) (SEQ ID NO:7), CG11151 gene product (AE003493) (SEQ ID NO:8) and CG12296 (AE003724) (SEQ ID NO:9). Yeast PXP-18 (D86472) SEQ ID NO:11) and C. elegans UNC-24 C-terminal portion (U42013) (SEQ ID NO:10). Consensus sequence is from the NCBI conserved domain search (RPS-BLAST 2.2.3). Position of the amino acid is labeled at the left side of the sequences. Amino acids represented as "*" are the consensus sequence of the SCP-2 sterol transfer domain and additional amino acids important for the sterol transfer function (Stolowich et al., 2002) as "+". Identical amino acid sequences between AeSCP-2 and other SCP-2 are represented as "▪". Gaps are introduced to maximize the alignment and are labeled as "-".

At page 38 of the specification, please replace the paragraph spanning lines 10-20 with the following replacement paragraph:

PCR amplification of the 5' cDNA end - Two primers were designed for 5' rapid amplification of cDNA end (RACE) based on the partial cDNA sequence AeSCP-2. Primer-1 (5'-GTCGGACTTCGAGAGACA-3' (SEQ ID NO:12)) and primer-2 (5'-TTACTTCAGCGAGG-3' (SEQ ID NO:13)) match to the N-terminal and the C-terminal of the protein, respectively. The Smart RACE cDNA amplification Kit (ClonTech, Palo Alto, CA) was used for 5' RACE with cDNAs made from 24 hour-old 4th instars. The PCR products were cloned into the pT-Adv plasmid (ClonTech), transformed into E. coli DH5 alpha strain and plated on LB plates under Ampicillin selection. Plasmid minipreps of 4 clones containing inserts were made using QiaSpin column (QIAGEN, Valencia, CA) and sequenced in an automatic sequencer (ABI 377XL) using BigDye labeling (Amersham Pharmacia Biotech AB, Uppsala, Sweden).

In the specification, please replace the paragraph spanning pg. 40, line 19 to pg. 41, line 8 with the following paragraph:

Western blotting analysis - Intact animals, dissected tissues and cultured tissues were homogenized in lysis buffer (0.25M TRIS® HCl (hydroxymethyl aminomethane hydrochloride) ~~Tris-HCl~~, pH 8.0/ 0.2% TRITON® X-100 (octyl phenol ethoxylate) ~~Triton X-100~~/ 1 mM dithioerythritol/ 5mM EDTA/ 10mM β-mercaptoethanol/ 1mM

phenylmethylsulfonyl fluoride/ protease inhibitor cocktail (Sigma)), and centrifuged at 12000 x g at 4°C for 15 minutes. Supernatants containing solvable proteins were stored at –80°C. Protein concentrations were determined using a BCA kit (Pierce, Rockford, IL). Western blotting analysis was performed as described (Lan et al., 1999) using either SDS 15% PAGE or SDS 4-20% gradient PAGE (ISC BioExpress, Kaysville, UT). The protein blots were incubated with 1:1500 dilution of rabbit polyclonal anti-AeSCP-2 antibodies. The goat anti-rabbit horseradish peroxidase conjugated secondary antibody (Jackson ImmunoResearch laboratory, West Grove, PA) was used at 1:3300 dilution. DAB solution (0.3 mg/ml and 0.03% hydrogen peroxide in PBS) was used to visualize the bound antibodies, which was developed within 5 minutes at room temperature.

In the specification at page 44, please replace line 21 with the following line:

FlyBase. 2001. [[http://]]flybase.bio.indiana.edu:82[[/]]

In the specification at page 47, please replace line 14 with the following line:

NCBI, 2002. [[http://]]www.ncbi.nlm.nih.gov/Structure/lexington/lexington.cgi